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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Kuber T. Sampath and Charles M. Cohen
- (ii) TITLE OF INVENTION: Methods For Tissue morphogenesis and Methods for Evaluating Morphogenic Activity
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: CREATIVE BIOMOLECULES, INC
  - (B) STREET: 45 SOUTH STREET
  - (C) CITY: HOPKINTON
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 01748
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Thomas C. Meyers
  - (B) REGISTRATION NUMBER: 36,989
  - (C) REFERENCE/DOCKET NUMBER: CRP-165
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (617) 248-7000
  - (B) TELEFAX: (617) 248-7100

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1822 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: HOMO SAPIENS
    - (F) TISSUE TYPE: HIPPOCAMPUS
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 49..1341
    - (C) IDENTIFICATION METHOD: experimental
    - (D) OTHER INFORMATION: /function= "MORPHOGENIC PROTEIN"
- /product= "OP1"
- /evidence= EXPERIMENTAL

GGT	GCG	GGG	GCC	CGG	AGC	CCC	GGG	GTA	GCG	CGT	AG	CGC	GCG	ATG	CAC	GTG	57
														Met	His	Val	
														1			
CGC	TCA	CTG	CGA	GCT	GCG	GCG	CCG	CAC	AGC	TTC	GTG	GCG	CTC	TGG	GCA		105
Arg	Ser	Leu	Arg	Ala	Ala	Ala	Pro	His	Ser	Phe	Val	Ala	Leu	Trp	Ala		
	5					10					15						
CCC	CTG	TTC	CTG	CTG	CGC	TCC	GCC	CTG	GCC	GAC	TTC	AGC	CTG	GAC	AAC		153
Pro	Leu	Phe	Leu	Leu	Arg	Ser	Ala	Leu	Ala	Asp	Phe	Ser	Leu	Asp	Asn		
20					25					30					35		
GAG	GTG	CAC	TCG	AGC	TTC	ATC	CAC	CGG	CGC	CTC	CGC	AGC	CAG	GAG	CGG		201
Glu	Val	His	Ser	Ser	Phe	Ile	His	Arg	Arg	Leu	Arg	Ser	Gln	Glu	Arg		
				40					45					50			
CGG	GAG	ATG	CAG	CGC	GAG	ATC	CTC	TCC	ATT	TTG	GGC	TTG	CCC	CAC	CGC		249
Arg	Glu	Met	Gln	Arg	Glu	Ile	Leu	Ser	Ile	Leu	Gly	Leu	Pro	His	Arg		
			55					60					65				
CCG	CGC	CCG	CAC	CTC	CAG	GGC	AAG	CAC	AAC	TCG	GCA	CCC	ATG	TTC	ATG		297
Pro	Arg	Pro	His	Leu	Gln	Gly	Lys	His	Asn	Ser	Ala	Pro	Met	Phe	Met		
		70					75					80					
CTG	GAC	CTG	TAC	AAC	GCC	ATG	GCG	GTG	GAG	GAG	GGC	GGC	GGG	CCC	GGC		345
Leu	Asp	Leu	Tyr	Asn	Ala	Met	Ala	Val	Glu	Glu	Gly	Gly	Gly	Pro	Gly		
	85					90					95						
GGC	CAG	GGC	TTC	TCC	TAC	CCC	TAC	AAG	GCC	GTC	TTC	AGT	ACC	CAG	GGC		393
Gly	Gln	Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	Thr	Gln	Gly		
100					105					110					115		
CCC	CCT	CTG	GCC	AGC	CTG	CAA	GAT	AGC	CAT	TTC	CTC	ACC	GAC	GCC	GAC		441
Pro	Pro	Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	Asp	Ala	Asp		
				120					125					130			
ATG	GTC	ATG	AGC	TTC	GTC	AAC	CTC	GTG	GAA	CAT	GAC	AAG	GAA	TTC	TTC		489
Met	Val	Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe		
			135				140						145				
CAC	CCA	CGC	TAC	CAC	CAT	CGA	GAG	TTC	CGG	TTT	GAT	CTT	TCC	AAG	ATC		537
His	Pro	Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile		
		150					155					160					
CCA	GAA	GGG	GAA	GCT	GTC	ACG	GCA	GCC	GAA	TTC	CGG	ATC	TAC	AAG	GAC		585
Pro	Glu	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp		
	165					170					175						
TAC	ATC	CGG	GAA	CGC	TTC	GAC	AAT	GAG	ACG	TTC	CGG	ATC	AGC	GTT	TAT		633
Tyr	Ile	Arg	Glu	Arg	Phe												

215

220

225

ATC Ile	ACA Thr	GCC Ala	ACC Thr	AGC Ser	AAC Asn	CAC His	TGG Trp	GTG Val	GTC Val	AAT Asn	CCG Pro	CGG Arg	CAC His	AAC Asn	CTG Leu	777
230																
GGC Gly	CTG Leu	CAG Gln	CTC Leu	TCG Ser	GTG Val	GAG Glu	ACG Thr	CTG Leu	GAT Asp	GGG Gly	CAG Gln	AGC Ser	ATC Ile	AAC Asn	CCC Pro	825
245																
AAG Lys	TTG Leu	GCG Ala	GGC Gly	CTG Leu	ATT Ile	GGG Gly	CGG Arg	CAC His	GGG Gly	CCC Pro	CAG Gln	AAC Asn	AAG Lys	CAG Gln	CCC Pro	873
260																
TTC Phe	ATG Met	GTG Val	GCT Ala	TTC Phe	TTC Phe	AAG Lys	GCC Ala	ACG Thr	GAG Glu	GTC Val	CAC His	TTC Phe	CGC Arg	AGC Ser	ATC Ile	921
280																
CGG Arg	TCC Ser	ACG Thr	GGG Gly	AGC Ser	AAA Lys	CAG Gln	CGC Arg	AGC Ser	CAG Gln	AAC Asn	CGC Arg	TCC Ser	AAG Lys	ACG Thr	CCC Pro	969
295																
AAG Lys	AAC Asn	CAG Gln	GAA Glu	GCC Ala	CTG Leu	CGG Arg	ATG Met	GCC Ala	AAC Asn	GTG Val	GCA Ala	GAG Glu	AAC Asn	AGC Ser	AGC Ser	1017
310																
AGC Ser	GAC Asp	CAG Gln	AGG Arg	CAG Gln	GCC Ala	TGT Cys	AAG Lys	AAG Lys	CAC His	GAG Glu	CTG Leu	TAT Tyr	GTC Val	AGC Ser	TTC Phe	1065
325																
CGA Arg	GAC Asp	CTG Leu	GGC Gly	TGG Trp	CAG Gln	GAC Asp	TGG Trp	ATC Ile	ATC Ile	GCG Ala	CCT Pro	GAA Glu	GGC Gly	TAC Tyr	GCC Ala	1113
340																
GCC Ala	TAC Tyr	TAC Tyr	TGT Cys	GAG Glu	GGG Gly	GAG Glu	TGT Cys	GCC Ala	TTC Phe	CCT Pro	CTG Leu	AAC Asn	TCC Ser	TAC Tyr	ATG Met	1161
360																
AAC Asn	GCC Ala	ACC Thr	AAC Asn	CAC His	GCC Ala	ATC Ile	GTG Val	CAG Gln	ACG Thr	CTG Leu	GTC Val	CAC His	TTC Phe	ATC Ile	AAC Asn	1209
375																
CCG Pro	GAA Glu	ACG Thr	GTG Val	CCC Pro	AAG Lys	CCC Pro	TGC Cys	TGT Cys	GCG Ala	CCC Pro	ACG Thr	CAG Gln	CTC Leu	AAT Asn	GCC Ala	1257
390																
ATC Ile	TCC Ser	GTC Val	CTC Leu	TAC Tyr	TTC Phe	GAT Asp	GAC Asp	AGC Ser	TCC Ser	AAC Asn	GTC Val	ATC Ile	CTG Leu	AAG Lys	AAA Lys	1305
405																
TAC Tyr	AGA Arg	AAC Asn	ATG Met	GTG Val	GTC Val	CGG Arg	GCC Ala	TGT Cys	GGC Gly	TGC Cys	CAC His	TAGCTCCTCC				1351
420																
425																
430																
GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG 1411																
GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG 1471																
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CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG 1711  
 GGC GTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC 1771  
 CTGTAATAAA TGTACAATA AAACGAATGA ATGAAAAAAA AAAAAAAAAA A 1822

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala  
 1 5 10 15  
 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser  
 20 25 30  
 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser  
 35 40 45  
 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu  
 50 55 60  
 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro  
 65 70 75 80  
 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly  
 85 90 95  
 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser  
 100 105 110  
 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr  
 115 120 125  
 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys  
 130 135 140  
 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu  
 145 150 155 160  
 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile  
 165 170 175  
 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile  
 180 185 190  
 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu  
 195 200 205  
 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu  
 210 215 220  
 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg  
 225 230 235 240

His	Asn	Leu	Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	
				245					250							
Ile	Asn	Pro	Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	
				260					265							
Lys	Gln	Pro	Phe	Met	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Phe	
				275					280							
Arg	Ser	Ile	Arg	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	
				290					295							
Lys	Thr	Pro	Lys	Asn	Gln	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	
				305					310							
Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	
				325					330							
Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	
				340					345							
Gly	Tyr	Ala	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	
				355					360							
Ser	Tyr	Met	Asn	Ala	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	His	
				370					375							
Phe	Ile	Asn	Pro	Glu	Thr	Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln	
				385					390							
Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	
				405					410							
Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala	Cys	Gly	Cys	His		
				420					425							

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Protein  
(B) LOCATION: 1..102  
(D) OTHER INFORMATION: /label= OPX

(xi) SEQUENCE DESCRIPTION: SEO ID NO:3:

Cys Xaa Xaa His Glu Leu Tyr Val Ser Phe Xaa Asp Leu Gly Trp Xaa  
1 5 10 15

Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly

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20	25	30
Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala		
35	40	45
Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys		
50	55	60
Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa		
65	70	75
Asp Xaa Ser Xaa Asn Val Ile Leu Xaa Lys Xaa Arg Asn Met Val Val		
85	90	95
Xaa Ala Cys Gly Cys His		
100		

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: /label= Generic-Seq-7

/note= "wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification."

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa Xaa Xaa Xaa Xaa Xaa		
1	5	10
Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Pro		
20	25	30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala Xaa Xaa Xaa Xaa Xaa		
35	40	45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Pro		
50	55	60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
65	70	75
Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Met Xaa Val Xaa Xaa Cys Xaa Cys		
85	90	95
Xaa		

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /label= Generic-Seq-8

/note= "wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Cys	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Gly	Trp	Xaa	1	5	10	15
Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Ala	Xaa	Tyr	Cys	Xaa	Gly	20	25	30	
Xaa	Cys	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	His	Ala	35	40	45	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	50	55	60	
Xaa	Cys	Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	65	70	75	80
Xaa	Xaa	Xaa	Xaa	Xaa	Val	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Met	Xaa	Val	85	90	95	
Xaa	Xaa	Cys	Xaa	Cys	Xaa											100			

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: /label= Generic-Seq-9

/note= "wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

[illegible]

(A) LENGTH: 102 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) NAME/KEY: Protein  
(B) LOCATION: 1..102  
(D) OTHER INFORMATION: /label= Generic-Seq-10

[illegible]



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## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Xaa Xaa Xaa Xaa  
1 5

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Cys Xaa Xaa Xaa Xaa  
1 5